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Dr. F. H. C. Crick, FRS,
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Dear Francis,

Some things which I forgot to include in yesterday's letter and some postscripts.

The histone octamer seems to be a pretty compact particle,* not very different from haemoglobin. The partial specific volume of most proteins is about 0.73 ml/g. Haemoglobin at 0.1M salt is .749 ml/g and in 2M salt is .779 ml/g. Jo Butler finds for the octamer in 2M salt .767 ml/g. This is very much in favour of the platysome model since the bipartite nucleosome one would be very open.

I enclose X-ray photos of the three main projections. I can't recall whether you have them with you or not. Notice that there are no strong 38 Å reflections, except in the hk0 plane. I think this must be the spacing between histones in the layers or turns of the platysome. Notice there is no 27 Å spacing in this plane.

The relation of the platysome to the nucleofilament and solenoid is still a mystery. If the platysomes are arranged with their planes at an angle to the nucleofilament axis there is less trouble about the mass per unit length (see enclosed photo of a "model" made by Michael Levitt) but the putative dyads would no longer be normal to the axis of the solenoid if this were maintained. However I rather like this type of model since this would explain the tendency of the nucleofilament to curl and coil. This model of course is unlike wedge-type ones, but there is "empty space" for H1.

A related question is the appearance of beads in electron micrographs. Nucleofilaments don't show any unless H1 is removed.. But Linda Sperling has found (in some experiments she was doing on the conditions for formation of solenoids) that if nucleofilaments, containing H1 extracted in .2 mM EDTA are put into as little as 15-30 mM sodium chloride, one suddenly sees beads,** whether one starts from nucleofilaments or from solenoids in the presence of magnesium.** My feeling is that this represents a kind of internal precipitation along the length of the nucleofilament which is reversible when the salt is dialysed out. On discussing these observations with Roger, he pointed out two things

that might be relevant to this idea of a bead precipitated out of an otherwise more or less continuous filament. 1) the fact that Georgiev finds that the tRNA stripping of histones H2A and H2B goes better in the absence of salt (i.e. in very low salt), contrary to commonsense, and 2) whereas sheared chromatin loses its micrococcal digestion pattern, the pattern isn't lost if the shearing is done in the presence of 5 mM magnesium and 100 mM sodium chloride (some unpublished experiments of Roger and Jean). Roger suggests that facts 1 and 2 go together, implying that added salt keeps H2A and H2B compactly on the nucleosome.

This makes me wonder whether the two layer or two turn platysome may not represent a somewhat collapsed structure, at least on the part of the DNA. After all DNAase I acting on chromatin doesn't show a pause at 140 base pairs and micrococcal shows a definite pause at 160. I wonder whether assigning 60 base pairs to the linker may not be too pat.

Are you going to Spetsai? I am pretty sure that I intend going this time, and I hope you can manage to get away from the Finland meeting to attend. I shan't imagine we would have much time at the Cold Spring Harbor meeting, and I don't think I can visit Aarhus, but will of course be at the Copenhagen meeting.

Yours ever,

Aaron

A. Klug

Encs.